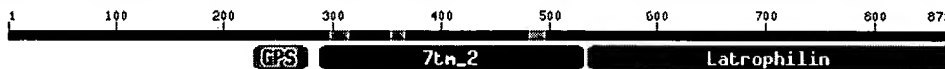


Your request has been successfully submitted and put into the Blast Queue.

Query = (872 letters)

Putative conserved domains have been detected, click on the image below for detailed results.



The request ID is

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Number of: Descriptions Alignments

Alignment view

Format for PSI-BLAST ☐ with inclusion threshold:

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Expect value range:

BLASTP 2.2.4 [Aug-26-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1032555785-026406-9303

Query=

(872 letters)

Database: All non-redundant GenBank CDS

translations+PDB+SwissProt+PIR+PRF

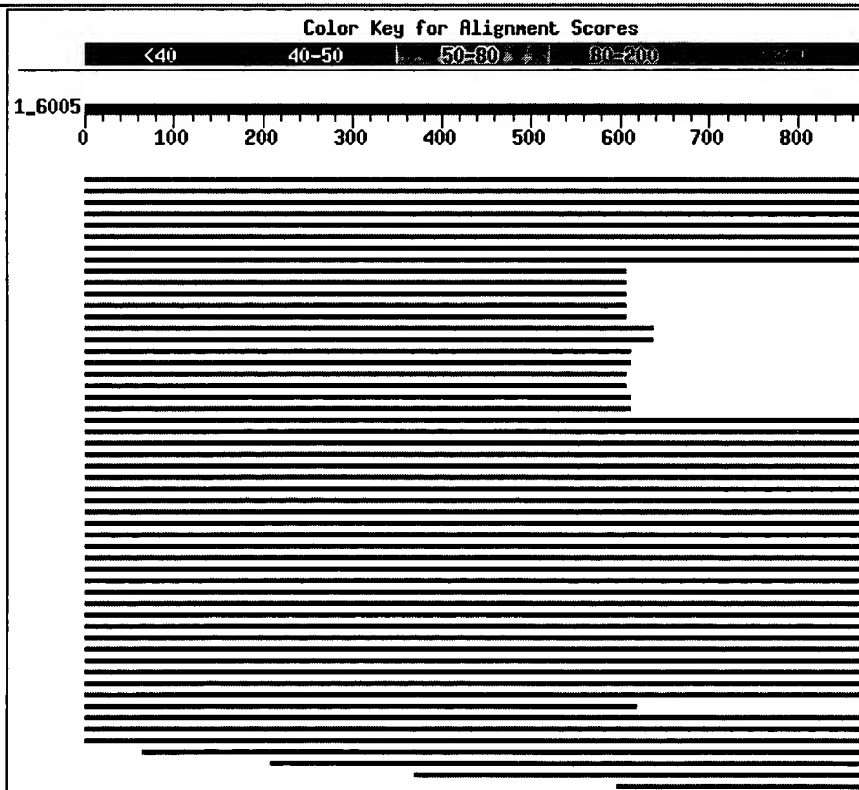
1,171,253 sequences; 370,891,306 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Score E
(bits) Value

Sequences producing significant alignments:

gi	3882257	dbj	BAA34488.1	(AB018311) KIAA0768 protein [Hom...	1659	0.0	L
gi	7513508	pir	T18395	latrophilin-3, splice variant bbaf, ...	1623	0.0	
gi	7513502	pir	T18389	latrophilin-3, splice variant abaf, ...	1620	0.0	
gi	7513949	pir	T17198	CL3BA protein - rat >gi 3695141 gb A...	1618	0.0	
gi	7513511	pir	T18407	latrophilin-3, splice variant bbbf, ...	1615	0.0	
gi	7513946	pir	T17186	CL3AA protein - rat >gi 3695135 gb A...	1613	0.0	
gi	7513505	pir	T18392	latrophilin-3, splice variant abbf, ...	1611	0.0	
gi	18677755	ref	NP 570835.1	(NM_130822) calcium-independen...	1600	0.0	L
gi	7513950	pir	T17199	CL3BB protein - rat >gi 3695143 gb A...	1118	0.0	
gi	7513947	pir	T17187	CL3AB protein - rat >gi 3695137 gb A...	1116	0.0	
gi	14149677	ref	NP 056051.1	(NM_015236) lectomedin-3 [Homo...	1116	0.0	L
gi	7513509	pir	T18398	latrophilin-3, splice variant bbag, ...	1115	0.0	
gi	7513503	pir	T18390	latrophilin-3, splice variant abag, ...	1115	0.0	
gi	7513951	pir	T17200	CL3BC protein - rat >gi 3695145 gb A...	1113	0.0	
gi	7513510	pir	T18405	latrophilin-3, splice variant bbah, ...	1112	0.0	
gi	7513948	pir	T17188	CL3AC protein - rat >gi 3695139 gb A...	1112	0.0	
gi	7513504	pir	T18391	latrophilin-3, splice variant abah, ...	1110	0.0	
gi	7513512	pir	T18408	latrophilin-3, splice variant bbbg, ...	1107	0.0	
gi	7513506	pir	T18393	latrophilin-3, splice variant abbg, ...	1107	0.0	
gi	7513513	pir	T18409	latrophilin-3, splice variant bbbh, ...	1104	0.0	
gi	7513507	pir	T18394	latrophilin-3, splice variant abbh, ...	1102	0.0	
gi	6912464	ref	NP 036434.1	(NM_012302) latrophilin 1; KIAA...	925	0.0	L
gi	7513498	pir	T18301	latrophilin-2, splice variant baaae ...	922	0.0	
gi	7513491	pir	T18381	latrophilin-2 (splice variant bbaae)...	922	0.0	
gi	7513487	pir	T18375	latrophilin-2 (splice variant babae)...	913	0.0	
gi	7513494	pir	T18385	latrophilin-2 (splice variant bbbae)...	913	0.0	
gi	7513500	pir	T18367	latrophilin-2, splice variant baabe ...	910	0.0	
gi	7513501	pir	T18383	latrophilin-2, splice variant bbabe ...	908	0.0	
gi	7513489	pir	T18379	latrophilin-2 (splice variant babbe)...	901	0.0	
gi	7513496	pir	T18387	latrophilin-2 (splice variant bbbbe)...	900	0.0	
gi	7513499	pir	T18366	latrophilin-2, splice variant baaaf ...	900	0.0	
gi	7513492	pir	T18382	latrophilin-2 (splice variant bbaaf)...	899	0.0	
gi	7513942	pir	T17158	CL2AB protein - rat >gi 3695125 gb A...	891	0.0	
gi	7513488	pir	T18377	latrophilin-2 (splice variant babaf)...	891	0.0	
gi	7513495	pir	T18386	latrophilin-2 (splice variant bbbaf)...	890	0.0	
gi	7513486	pir	T18370	latrophilin-2 (splice variant baabf)...	887	0.0	
gi	3882293	dbj	BAA34506.1	(AB018329) KIAA0786 protein [Hom...	887	0.0	L
gi	7513493	pir	T18384	latrophilin-2 (splice variant bbabf)...	887	0.0	
gi	11280659	pir	T46611	CL2BB protein - rat >gi 3695131 gb ...	879	0.0	
gi	7513490	pir	T18380	latrophilin-2 (splice variant babbf)...	879	0.0	
gi	7513497	pir	T18388	latrophilin-2 (splice variant bbbbf)...	878	0.0	
gi	7513943	pir	T17159	CL2AC protein - rat >gi 3695127 gb A...	870	0.0	
gi	7513941	pir	T17157	CL2AA protein - rat >gi 3695123 gb A...	862	0.0	
gi	7513945	pir	T17185	CL2BC protein - rat >gi 3695133 gb A...	857	0.0	
gi	19705539	ref	NP 599235.1	(NM_134408) calcium-independen...	852	0.0	L
gi	7513944	pir	T17160	CL2BA protein - rat >gi 3695129 gb A...	849	0.0	
gi	5880490	gb	AAD54675.1	AF104266 1 (AF104266) lectomedin-1...	736	0.0	L
gi	12621148	ref	NP 075251.1	(NM_022962) CL1BA protein [Rat...	709	0.0	L
gi	7513937	pir	T17138	CL1AA protein - rat >gi 2213659 gb A...	709	0.0	
gi	7513485	pir	T18413	latrophilin-1, brain-specific - bovi...	702	0.0	
gi	7513484	pir	T18411	latrophilin-1, brain-specific - bovi...	702	0.0	
gi	7662324	ref	NP 055736.1	(NM_014921) lectomedin-2; KIAA0...	701	0.0	L
gi	11037014	gb	AAG27461.1	AF307079 1 (AF307079) lectomedin-...	701	0.0	L
gi	7513940	pir	T17156	CL1BB protein - rat >gi 3695121 gb A...	689	0.0	
gi	7513938	pir	T17145	CL1AB protein - rat >gi 3695117 gb A...	689	0.0	
gi	5880492	gb	AAD54676.1	AF104938 1 (AF104938) lectomedin-1...	677	0.0	L
gi	14043198	gb	AAH07587.1	AAH07587 (BC007587) Unknown (prot...	643	0.0	L
gi	20885613	ref	XP 134383.1	(XM_134383) similar to CL1BA p...	523	e-147	L
gi	20878925	ref	XP 131258.1	(XM_131258) similar to phospho...	503	e-141	L
gi	20835942	ref	XP 144383.1	(XM_144383) similar to beta-ca...	494	e-138	L

gi	11545908	ref	NP_071442.1	(NM_022159)	EGF-TM7-latrophili...	311	2e-83	L
gi	18875378	ref	NP_573485.1	(NM_133222)	ETL1 [Mus musculus...	300	5e-80	L
gi	16877798	gb	AAH17134.1	(BC017134)	Unknown (protein for ...	299	1e-79	L
gi	20879033	ref	XP_124185.1	(XM_124185)	similar to ETL1 [M...	299	1e-79	L
gi	11560111	ref	NP_071630.1	(NM_022294)	ETL protein [Rattu...	287	6e-76	L
gi	20835937	ref	XP_144382.1	(XM_144382)	similar to calcium...	237	4e-61	L
gi	9663052	emb	CAC01096.1	(AJ272270)	110-R orphan receptor...	228	2e-58	
gi	14211883	ref	NP_115960.1	(NM_032571)	EGF-like module-co...	227	5e-58	L
gi	15528829	gb	AAK51125.1	(AY032690)	EGF-like module-conta...	223	1e-56	L
gi	20982827	ref	NP_631877.1	(NM_139138)	F4/80-like-recepto...	223	1e-56	L
gi	20900604	ref	XP_128711.1	(XM_128711)	EGF-like module co...	215	2e-54	L
gi	17978489	ref	NP_001775.2	(NM_001784)	CD97 antigen, isof...	212	2e-53	L
gi	17978491	ref	NP_510966.1	(NM_078481)	CD97 antigen, isof...	211	3e-53	L
gi	1685051	gb	AAB36682.1	(U76764)	CD97 [Homo sapiens]	211	3e-53	L
gi	19170724	emb	CAC94754.1	(AJ416058)	CD97 protein [Bos ta...	211	3e-53	
gi	21929208	dbj	BAC06178.1	(AB065966)	seven transmembrane ...	211	4e-53	
gi	17531351	ref	NP_495894.1	(NM_063493)	G-protein coupled ...	210	6e-53	L
gi	11225481	gb	AAG33020.1	(AF192402)	ETL protein [Rattus n...	209	1e-52	L
gi	2135556	pir	I37225	leucocyte antigen CD97 - human	>gi 8...	207	7e-52	
gi	6226566	sp	P48960	CD97 HUMAN	Leucocyte antigen CD97 prec...	206	1e-51	
gi	7305025	ref	NP_038475.1	(NM_013447)	egf-like module con...	198	3e-49	L
gi	21929123	dbj	BAC06146.1	(AB065931)	seven transmembrane ...	197	4e-49	
gi	22024081	ref	NP_610397.2	(NM_136553)	CG8639 gene produc...	192	1e-47	L
gi	4469185	emb	CAB38413.1	(AL031588)	dJ1163J1.1 (mostly su...	192	2e-47	L
gi	7656967	ref	NP_055061.1	(NM_014246)	cadherin EGF LAG se...	191	4e-47	L
gi	2935597	gb	AAC05172.1	(AC004262)	R29368_2 [Homo sapiens]	191	5e-47	L
gi	6753408	ref	NP_034016.1	(NM_009886)	cadherin EGF LAG se...	188	3e-46	L
gi	7021080	dbj	BAA91375.1	(AK000781)	unnamed protein produ...	185	2e-45	
gi	15638633	gb	AAL05061.1	AF413207_1	(AF413207) CD97 antige...	181	3e-44	
gi	21929097	dbj	BAC06133.1	(AB065918)	seven transmembrane ...	180	7e-44	
gi	4503565	ref	NP_001965.1	(NM_001974)	egf-like module con...	177	4e-43	L
gi	22095545	sp	Q9QYP2	CLR2 RAT	Cadherin EGF LAG seven-pass ...	176	9e-43	
gi	7707357	gb	AAF67800.1	AF146344_1	(AF146344) CD97 antigen...	174	6e-42	L
gi	13529572	gb	AAH05499.1	(BC005499)	Unknown (protein for ...	174	6e-42	L
gi	12835843	dbj	BAB23386.1	(AK004577)	CD97 antigen-data so...	173	9e-42	L
gi	13879392	gb	AAH06676.1	(BC006676)	Similar to CD97 antig...	173	9e-42	L
gi	1665821	dbj	BAA13407.1	(D87469)	Similar to D.melanogast...	173	1e-41	L
gi	13325064	ref	NP_001399.1	(NM_001408)	cadherin EGF LAG s...	172	1e-41	L
gi	22095553	sp	Q9ROM0	CLR2 MOUSE	Cadherin EGF LAG seven-pas...	172	2e-41	
gi	11995466	ref	NP_059088.1	(NM_017392)	cadherin EGF LAG s...	171	3e-41	L

Alignments

Get selected sequences

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☐ >gi|3882257|dbj|BAA34488.1| (AB018311) KIAA0768 protein [Homo sapiens]
Length = 872

Score = 1659 bits (4296), Expect = 0.0

Identities = 818/872 (93%), Positives = 818/872 (93%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKAMVETVNNLLQP 60

AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKAMVETVNNLLQP

Sbjct: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKAMVETVNNLLQP 60

Query: 61 QALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120

QALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG

Sbjct: 61 QALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTDNIKLEVARLSTEG 120

Query: 121 NLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYLSTENASMKLGTEA 180
 NLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYLSTENASMKLGTEA
 Sbjct: 121 NLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYLSTENASMKLGTEA 180

Query: 181 LSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFNPNCFSWSYSKRTM 240
 LSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFNPNCFSWSYSKRTM
 Sbjct: 181 LSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFNPNCFSWSYSKRTM 240

Query: 241 TGYWSTNGCRLLTTNKTHTTTCSCNHLTNFAVLMAHVEVKHSDAVHDLDDLVDITWVGXXXX 300
 TGYWST GCRLLTTNKTHTTTCSCNHLTNFAVLMAHVEVKHSDAVHDLDDLVDITWVG
 Sbjct: 241 TGYWSTQGCRLLTTNKTHTTTCSCNHLTNFAVLMAHVEVKHSDAVHDLDDLVDITWVGILLS 300

Query: 301 XXXXXXXXXXXXXXXXRG LNSDRNTIHKNLCSL FVAELLFLIGINRTDQPIACXXXXXXXXX 360
 RGL SDRNTIHKNLCSL FVAELLFLIGINRTDQPIAC
 Sbjct: 301 LVCLLICIFTFCFFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTDQPIACAVFAALLH 360

Query: 361 XXXXXXXXTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIVAVSAAVDYRSYGT 420
 TWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIVAVSAAVDYRSYGT
 Sbjct: 361 FFFLAATWWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIVAVSAAVDYRSYGT 420

Query: 421 DKVCWLRRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKPESGCLDNIKSWVI 480
 DKVCWLRRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKPESGCLDNIKSWVI
 Sbjct: 421 DKVCWLRRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKPESGCLDNIKSWVI 480

Query: 481 XXXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHCVLQKKVRKEYGKC 540
 MYINESTVIMAYLFTIFNSL GMFIFIFHCVLQKKVRKEYGKC
 Sbjct: 481 GAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVRKEYGKC 540

Query: 541 LRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSNSRIRRMWNDTVRKQSESSFITGDINS 600
 LRTHCCSGKSTESSIGSGKTSGRTPGRYSTGS SRIRRMWNDTVRKQSESSFITGDINS
 Sbjct: 541 LRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSQSRIRRMWNDTVRKQSESSFITGDINS 600

Query: 601 SASLNREGLLNARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEK 660
 SASLNREGLLNARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEK
 Sbjct: 601 SASLNREGLLNARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEK 660

Query: 661 KILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVLDDATSFNHEESLG 720
 KILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVLDDATSFNHEESLG
 Sbjct: 661 KILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVLDDATSFNHEESLG 720

Query: 721 LELIHEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDS 780
 LELIHEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDS
 Sbjct: 721 LELIHEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDS 780

Query: 781 LYTSMPFLAGVAATESVTTSTQTETPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLG 840
 LYTSMPFLAGVAATESVTTSTQTETPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLG
 Sbjct: 781 LYTSMPFLAGVAATESVTTSTQTETPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLG 840

Query: 841 RGSSDGFIVPPNKDGTPEGSSKGAHLVTSL 872
 RGSSDGFIVPPNKDGTPEGSSKGAHLVTSL
 Sbjct: 841 RGSSDGFIVPPNKDGTPEGSSKGAHLVTSL 872

☐ >gi|7513508|pir||T18395 latrophilin-3, splice variant bbaf, brain-specific - bov
 gi|4164065|gb|AAD05327.1| (AF111091) latrophilin 3 splice variant bbaf [Bos tauru
 Length = 1571

Score = 1623 bits (4202), Expect = 0.0
 Identities = 807/928 (86%), Positives = 810/928 (86%), Gaps = 56/928 (6%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK
 Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVMNLLQPQALNAWRDLTTS DQLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107

AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 763
 Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
 NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
 Sbjct: 764 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 823
 Query: 168 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
 STENASMKLGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
 Sbjct: 824 STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 883
 Query: 228 PNCSEFWSYSKRTMTGYWSTNGCRLLTTNKTHHTTSCCNHLTNFAVLMAHVEVKHSDAVHDL 287
 PNCSEFWSYSKRTMTGYWST GCRLLTTNKTHHTTSCCNHLTNFAVLMAHVEVKHSDAVHDL
 Sbjct: 884 PNCSEFWSYSKRTMTGYWSTQGCRLLTTNKTHHTTSCCNHLTNFAVLMAHVEVKHSDAVHDL 943
 Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXXXXXRG LNSDRNTIHKNLCSL FVAELLFLIGINRTD 347
 LLDVITWVG RGL SDRNTIHKNLCSL FVAELLFLIGINRTD
 Sbjct: 944 LLDVITWVGILLSLVCLLICITFCFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTD 1003
 Query: 348 QPIACXXXXXXXXXXXXXXXXXTW MFLEGVQLYIMLVEVFESEHSRRKYFYLVGYGMPALIV 407
 QPIAC TW MFLEGVQLYIMLVEVFESEHSRRKYFYLVGYGMPALIV
 Sbjct: 1004 QPIACAVFAALLHFFFLAAFTW MFLEGVQLYIMLVEVFESEHSRRKYFYLVGYGMPALIV 1063
 Query: 408 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 467
 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP
 Sbjct: 1064 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 1123
 Query: 468 ESGCLDNIKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHC 527
 ESGCLDNIKSWVI MYINESTVIMAYLFTIFNSL GMFIFIFHC
 Sbjct: 1124 ESGCLDNIKSWVIGAIALLCLLGLT WAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHC 1183
 Query: 528 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSNSRIRRMWNDTVRK 587
 VLQKKVRKEYGKCLRTHCCSG+STESSIGSGKTSGRTPGRYSTGS SRIRRMWNDTVRK
 Sbjct: 1184 VLQKKVRKEYGKCLRTHCCSGRSTESSIGSGKTSGRTPGRYSTGSQSRIIRRMWNDTVRK 1243
 Query: 588 QSESSFITGDINSSASLNR----- 606
 QSESSFITGDINSSASLNR
 Sbjct: 1244 QSESSFITGDINSSASLNRGAMANHLISNALLRPHGTNNPYN TLLGEPAVCNNPSVSMYN 1303
 Query: 607 --EGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQI IDRGYNHNETALEKKILK 664
 EGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQI IDRGYNHNETALEKKILK
 Sbjct: 1304 AQEGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQI IDRGYNHNETALEKKILK 1363
 Query: 665 ELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVLDDATSFNHEESLGLELI 724
 ELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS EDDAIVLDDATSFNHEESLGLELI
 Sbjct: 1364 ELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS EDDAIVLDDATSFNHEESLGLELI 1423
 Query: 725 HEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS 784
 HEESDAPLLPPRVYSTENHQ HHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS
 Sbjct: 1424 HEESDAPLLPPRVYSTENHQLHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS 1483
 Query: 785 MPTLAGVAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS 844
 MP LAGV ESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS
 Sbjct: 1484 MPALAGVPTAESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS 1543
 Query: 845 DGFIVPPNKDGTTPPEGSSKGP AHLVTS L 872
 DGFIVPPNKDGTTPPEGSSKGP AHLVTS L
 Sbjct: 1544 DGFIVPPNKDGTTPPEGSSKGP AHLVTS L 1571

☐ >gi|7513502|pir|T18389 latrophilin-3, splice variant abaf, brain-specific - bov
 gi|4164053|gb|AAD05321.1| (AF111085) latrophilin 3 splice variant abaf [Bos taurus
 Length = 1503

Score = 1620 bits (4195), Expect = 0.0
 Identities = 807/928 (86%), Positives = 810/928 (86%), Gaps = 56/928 (6%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
 Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK 635

Query: 49 -AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
 NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
 Sbjct: 696 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 755

Query: 168 STENASMKGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
 STENASMKGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
 Sbjct: 756 STENASMKGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 815

Query: 228 PNCFSWSYSKRTMTGYWSTNGCRLLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 287
 PNCFSWSYSKRTMTGYWST GCRLLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL
 Sbjct: 816 PNCFSWSYSKRTMTGYWSTQGCRLLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 875

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXXXXXRGNSDRNTIHKNLCSLFAELLFLIGINRTD 347
 LLDVITWVG RGL SDRNTIHKNLCSLFAELLFLIGINRTD
 Sbjct: 876 LLDVITWVGILLSLVCLLICIFTFCFRGLQSDRNTIHKNLCSLFAELLFLIGINRTD 935

Query: 348 QPIACXXXXXXXXXXXXXXXXXTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 407
 QPIAC TWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV
 Sbjct: 936 QPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 995

Query: 408 AVSAAVDYRSYGTDKVCWLRLDITYFIWSFIGPATLIIMLNVIFLGIALYKMFHHTAILKP 467
 AVSAAVDYRSYGTDKVCWLRLDITYFIWSFIGPATLIIMLNVIFLGIALYKMFHHTAILKP
 Sbjct: 996 AVSAAVDYRSYGTDKVCWLRLDITYFIWSFIGPATLIIMLNVIFLGIALYKMFHHTAILKP 1055

Query: 468 ESGCLDNIKSWVIXXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHC 527
 ESGCLDNIKSWVI MYINESTVIMAYLFTIFNSL GMFIFIFHC
 Sbjct: 1056 ESGCLDNIKSWVIGAIALLCLLGLTWAFLMYINESTVIMAYLFTIFNSLQGMFIFIFHC 1115

Query: 528 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSNSRIRRMWNDTVRK 587
 VLQKKVRKEYGKCLRTHCCSG+STESSIGSGKTSGRTPGRYSTGS SRIRRMWNDTVRK
 Sbjct: 1116 VLQKKVRKEYGKCLRTHCCSGRSTESSIGSGKTSGRTPGRYSTGSQSRIRRMWNDTVRK 1175

Query: 588 QSESSFITGDINSSASLNR----- 606
 QSESSFITGDINSSASLNR
 Sbjct: 1176 QSESSFITGDINSSASLNRGAMANHLISNALLRPHGTNNPYNTLLGEPACNNPSVSMYN 1235

Query: 607 --EGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK 664
 EGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK
 Sbjct: 1236 AQEGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILK 1295

Query: 665 ELTSNYIPSYLNNHERSSEQNRNLMNKLVNNLGSGREDDAIVLDDATSFNHEESLGLELI 724
 ELTSNYIPSYLNNHERSSEQNRNLMNKLVNNLGSG EDDAIVLDDATSFNHEESLGLELI
 Sbjct: 1296 ELTSNYIPSYLNNHERSSEQNRNLMNKLVNNLGSGSEDDAIVLDDATSFNHEESLGLELI 1355

Query: 725 HEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS 784
 HEESDAPLLPPRVYSTENHQ HHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS
 Sbjct: 1356 HEESDAPLLPPRVYSTENHQLHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTS 1415

Query: 785 MPTLAGVAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS 844
 MP LAGV ESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS
 Sbjct: 1416 MPALAGVPTAESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSS 1475

Query: 845 DGFIVPPNKDGTPEGSSKGAHLVTS 872
 DGFIVPPNKDGTPEGSSKGAHLVTS
 Sbjct: 1476 DGFIVPPNKDGTPEGSSKGAHLVTS 1503

☐ >gi|7513949|pir|T17198 CL3BA protein - rat
 gi|3695141|gb|AAC62663.1 (AF081157) CL3BA [Rattus norvegicus]
 Length = 1527

Score = 1618 bits (4189), Expect = 0.0
 Identities = 791/885 (89%), Positives = 801/885 (90%), Gaps = 13/885 (1%)

```

Query: 1      AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNK----- 48
              AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNK
Sbjct: 643    AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTTPGGKDSAARSLNKLQKRERSCRAYV 702

Query: 49     -AMVETVNNLLQPQALNAWRDLTTS DQLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
              AMVETVNNLLQPQALNAWRDLTTS DQLRAATMLL TVEESAFVLADNLLKTDIVRENTD
Sbjct: 703    QAMVETVNNLLQPQALNAWRDLTTS DQLRAATMLLD TVEESAFVLADNLLKTDIVRENTD 762

Query: 108    NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
              NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
Sbjct: 763    NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 822

Query: 168    STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
              STENASMKLGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
Sbjct: 823    STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 882

Query: 228    PNCSEFWSYSKRTMTGYWSTNGCRLLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL 287
              PNCSEFWSYSKRTMTGYWST GCRLLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL
Sbjct: 883    PNCSEFWSYSKRTMTGYWSTQGCRLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL 942

Query: 288    LLDVITWVGXXXXXXXXXXXXXXXXXXXXXRG LNSDRNTIHKNLCSL FVAELLFLIGINRTD 347
              LLDVITWVG RGL SDRNTIHKNLCSL FVAELLFLIGINRTD
Sbjct: 943    LLDVITWVGILLSLVCLLICIFTFCFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTD 1002

Query: 348    QPIACXXXXXXXXXXXXXXXXXXXTW MFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 407
              QPIAC TW MFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV
Sbjct: 1003   QPIACAVFAALLHFFFLAAFTW MFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 1062

Query: 408    AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 467
              AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP
Sbjct: 1063   AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 1122

Query: 468    ESGCLDNIKSWVIXXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHC 527
              ESGCLDNIKSWVI MYINESTVIMAYLFTIFNSL GMFIFIFHC
Sbjct: 1123   ESGCLDNIKSWVIGAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHC 1182

Query: 528    VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGSNSRIRRMWNDTVRK 587
              VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGS SRIRRMWNDTVRK
Sbjct: 1183   VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGSQSRIIRRMWNDTVRK 1242

Query: 588    QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQII 647
              QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIA GEYLSNCVQII
Sbjct: 1243   QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIAGGEYLSNCVQII 1302

Query: 648    DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGS GREDDAIVL 707
              DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRN+MNKL V+NLGSG EDDAIVL
Sbjct: 1303   DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRNMMNKLVDNLGSGSEDDAIVL 1362

Query: 708    DDATSFNHEESLGLLELIHEESDAPLLP PRVYSTENHQP HHYTRRRIPQDHSESFFPLLTN 767
              DDA SFNHEESLGLLELIHEESDAPLLP PRVYST+NHQP HHY+RRR+PQDHSESFFPLLT+
Sbjct: 1363   DDAASFNHEESLGLLELIHEESDAPLLP PRVYSTDNHQP HHYSRRRLPQDHSESFFPLLT D 1422

Query: 768    EHTEDLQSPHRDSLYTSMPTLAGVAATESVT TSTQTETPPPAKCGDAEDVYYKSM PNLGSR 827
              EHTED QSPHRDSLYTSMPT LAGV A +SVTTSTQTE AK GDAEDVYYKSM PNLGSR
Sbjct: 1423   EHTEDPQSPHRDSLYTSMPTALAGVPAADSVTTSTQTEAAAAKGGDAEDVYYKSM PNLGSR 1482

Query: 828    NHVHQLHTYYQLGRGSSDGFIVPPNKDGT PPEGSSSKGPAHLVTSL 872
              NHVH LH YYQLGRGSSDGFIVPPNKDG PEG+SKGPAHLVTSL
  
```


Sbjct: 1483 NHVHPLHAYYQLGRGSSDGFIVPPNKDGASPEGTSKGAHLVTSL 1527

☐ >gi|7513511|pir||T18407 latrophilin-3, splice variant bbbf, brain-specific - bov
gi|4164071|gb|AAD05330.1 (AF111094) latrophilin 3 splice variant bbbf [Bos taurus
Length = 1580

Score = 1615 bits (4181), Expect = 0.0

Identities = 807/937 (86%), Positives = 810/937 (86%), Gaps = 65/937 (6%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK
Sbjct: 644 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKLQKRERSCRAYV 703

Query: 49 -AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD
Sbjct: 704 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLDTVESAFVLADNLLKTDIVRENTD 763

Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
Sbjct: 764 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 823

Query: 168 STENASMKLGTEALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
STENASMKLGTEA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
Sbjct: 824 STENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 883

Query: 228 PNCSEFWSYSKRTMTGYWSTNGCRLLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL 287
PNCSEFWSYSKRTMTGYWST GCRLLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL
Sbjct: 884 PNCSEFWSYSKRTMTGYWSTQGCRLLTTNKTHTTCSNHLTNFAVLMAHVEVKHSDAVHDL 943

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXRG LNSDRNTIHKNLCSL FVAELLFLIGINRTD 347
LLDVITWVG RGL SDRNTIHKNLCSL FVAELLFLIGINRTD
Sbjct: 944 LLDVITWVGILLSLVCLLICIFTFCFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTD 1003

Query: 348 QPIACXXXXXXXXXXXXXXXXXTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 407
QPIAC TWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV
Sbjct: 1004 QPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 1063

Query: 408 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 467
AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP
Sbjct: 1064 AVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 1123

Query: 468 ESGCLDN-----IKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLN 518
ESGCLDN IKSWVI MYINESTVIMAYLFTIFNSL
Sbjct: 1124 ESGCLDNINYEDNRPFIKSWVIGAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQ 1183

Query: 519 GMFIFIFHCVLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGSRTPGRYSTGSNSRIR 578
GMFIFIFHCVLQKKVRKEYGKCLRTHCCSG+STESSIGSGKTSGSRTPGRYSTGS SRIR
Sbjct: 1184 GMFIFIFHCVLQKKVRKEYGKCLRTHCCSGRSTESSIGSGKTSGSRTPGRYSTGSQSRIR 1243

Query: 579 RMWNDTVRKQSESSFITGDINSSASLNR----- 606
RMWNDTVRKQSESSFITGDINSSASLNR
Sbjct: 1244 RMWNDTVRKQSESSFITGDINSSASLNRGAMANHLISNALLRPHGTNNPYNTLLGEPAVC 1303

Query: 607 -----EGLLN NARDTSVMDTLP L NGNHGNSSYSIASGEYLSNCVQIIDRGYNHNE 655
EGLLN NARDTSVMDTLP L NGNHGNSSYSIASGEYLSNCVQIIDRGYNHNE
Sbjct: 1304 NNPSVSMYNAQEGLLN NARDTSVMDTLP L NGNHGNSSYSIASGEYLSNCVQIIDRGYNHNE 1363

Query: 656 TALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNL GSGREDDAIVLDDATSFNH 715
TALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNL GSG EDDAIVLDDATSFNH
Sbjct: 1364 TALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNL GSG SEDDAIVLDDATSFNH 1423

Query: 716 EESLGLELIHEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTNEHTEDLQS 775
EESLGLELIHEESDAPLLPPRVYSTENHQ HHYTRRRIPQDHSESFFPLLTNEHTEDLQS
Sbjct: 1424 EESLGLELIHEESDAPLLPPRVYSTENHQLHHYTRRRIPQDHSESFFPLLTNEHTEDLQS 1483

Query: 776 PHRDSLYTSMPTLAGVAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHT 835
 PHRDSLYTSMP LAGV ESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHT
 Sbjct: 1484 PHRDSLYTSMPALAGVPTAESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHT 1543

Query: 836 YYQLGRGSSDGFIVPPNKGDTPEEGSSKGAHLVTS 872
 YYQLGRGSSDGFIVPPNKGDTPEEGSSKGAHLVTS
 Sbjct: 1544 YYQLGRGSSDGFIVPPNKGDTPEEGSSKGAHLVTS 1580

☐ >gi|7513946|pir|T17186 CL3AA protein - rat
 gi|3695135|gb|AAC62660.1| (AF081154) CL3AA [Rattus norvegicus]
 Length = 1459

Score = 1613 bits (4178), Expect = 0.0
 Identities = 791/885 (89%), Positives = 801/885 (90%), Gaps = 13/885 (1%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK
 Sbjct: 575 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKLQKRERSCRAYV 634

Query: 49 -AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
 AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD
 Sbjct: 635 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 694

Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
 NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL
 Sbjct: 695 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 754

Query: 168 STENASMKLGTALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
 STENASMKLGTAA+STNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN
 Sbjct: 755 STENASMKLGTAASTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 814

Query: 228 PNCFSWSYSKRTMTGYWSTNGCRLLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL 287
 PNCFSWSYSKRTMTGYWST GCRLLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL
 Sbjct: 815 PNCFSWSYSKRTMTGYWSTQGCRLTTNKTHTTSCSNHLTNFAVLMAHVEVKHSDAVHDL 874

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXRG LNSDRNTIHKNLCSL FVAELLFLIGINRTD 347
 LLDVITWVG RGL SDRNTIHKNLCSL FVAELLFLIGINRTD
 Sbjct: 875 LLDVITWVGILLSLVCLLICIFTFCFFRGLQSDRNTIHKNLCSL FVAELLFLIGINRTD 934

Query: 348 QPIACXXXXXXXXXXXXXXXXXTW MFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 407
 QPIAC TW MFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV
 Sbjct: 935 QPIACAVFAALLHFFFLAAFTW MFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 994

Query: 408 AVSAAVDYRSYGTDKVCWLRLD TYFIW SFIPATLIIMLNVI FLGIALYKMFHHTAILKP 467
 AVSAAVDYRSYGTDKVCWLRLD TYFIW SFIPATLIIMLNVI FLGIALYKMFHHTAILKP
 Sbjct: 995 AVSAAVDYRSYGTDKVCWLRLD TYFIW SFIPATLIIMLNVI FLGIALYKMFHHTAILKP 1054

Query: 468 ESGCLDNIKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLNGMFIFIFHC 527
 ESGCLDNIKSWVI MYINESTVIMAYLFTIFNSL GMFIFIFHC
 Sbjct: 1055 ESGCLDNIKSWVIGAIALLC LLGLTWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHC 1114

Query: 528 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGS NRIRRMWNDTVRK 587
 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGS SRIRRMWNDTVRK
 Sbjct: 1115 VLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTS GSRTPGRYSTGS QSRIIRRMWNDTVRK 1174

Query: 588 QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQII 647
 QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIA GEYLSNCVQII
 Sbjct: 1175 QSESSFITGDINSSASLNREGLLN NARDTSVMDTLPLNGNHGNSYSIAGGEYLSNCVQII 1234

Query: 648 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRNLMNKL VNNLGSGREDDAIVL 707
 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRN+MNKL V+NLGSG EDDAIVL
 Sbjct: 1235 DRGYNHNETALEKKILKELTSNYIPSYLNNHERSSEQNRNMMNKLVDNLGSGSEDDAIVL 1294

Query: 708 DDATSFNHEESLGLLELIEESDAPLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLTN 767
 DDA SFNHEESLGLLELIEESDAPLLPPRVYST+NHQPHHY+RRR+PQDHSESFFPLLT+

Sbjct: 1295 DDAASFNHEESLGLELIHEESDAPLLPPRVYSTDNHQPHYSRRRLPQDHSESFFPLLT 1354

Query: 768 EHTEDLQSPHRDSLYTSMPTLAGVAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGS 827
EHTED QSPHRDSLYTSMPT LAGV A +SVTTSTQTE AK GDAEDVYYKSMPNLGS

Sbjct: 1355 EHTEDPQSPHRDSLYTSMPALAGVPAADSVTTSTQTEAAAAKGGDAEDVYYKSMPNLGS 1414

Query: 828 NHVHQLHTYYQLGRGSSDGFIVPPNKGDTPEGSSSKGPAHLVTSL 872
NHVH LH YYQLGRGSSDGFIVPPNKG PEG+SKGPAHLVTSL

Sbjct: 1415 NHVHPLHAYYQLGRGSSDGFIVPPNKGASPEGTSKGPAHLVTSL 1459

☐ >gi|7513505|pir|T18392 latrophilin-3, splice variant abbf, brain-specific - bov
gi|4164059|gb|AAD05324.1 (AF111088) latrophilin 3 splice variant abbf [Bos tauru
Length = 1512

Score = 1611 bits (4171), Expect = 0.0
Identities = 807/937 (86%), Positives = 810/937 (86%), Gaps = 65/937 (6%)

Query: 1 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK----- 48
AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNK

Sbjct: 576 AEQTRNHLNAGDITYSVRAMDQLVGLLDVQLRNLTPGGKDSAARSLNKLQKRERSCRAYV 635

Query: 49 -AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLHTVEESAFVLADNLLKTDIVRENTD 107
AMVETVNNLLQPQALNAWRDLTTSQDLRAATMLL TVEESAFVLADNLLKTDIVRENTD

Sbjct: 636 QAMVETVNNLLQPQALNAWRDLTTSQDLRAATMLLDTVEESAFVLADNLLKTDIVRENTD 695

Query: 108 NIKLEVARLSTEGNLEDLKFPENMGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 167
NI+LEVARLSTEGNLEDLKFPEN GHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL

Sbjct: 696 NIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGEIRVAFVLYNNLGPYL 755

Query: 168 STENASMKLGTALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 227
STENASMKLGTALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN

Sbjct: 756 STENASMKLGTALSTNHSVIVNSPVITAAINKEFSNKVYLADPVVFTVKHIKQSEENFN 815

Query: 228 PNCSFWSYSKRTMTGYWSTNGCRLLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 287
PNCSFWSYSKRTMTGYWST GCRLLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL

Sbjct: 816 PNCSFWSYSKRTMTGYWSTQGCRLLTTNKTHHTCSCNHLTNFAVLMAHVEVKHSDAVHDL 875

Query: 288 LLDVITWVGXXXXXXXXXXXXXXXXXRGNSDRNTIHKNLCSLFAELLFLIGINRTD 347
LLDVITWVG RGL SDRNTIHKNLCSLFAELLFLIGINRTD

Sbjct: 876 LLDVITWVGILLSLVCLLICIFTFCFRGLQSDRNTIHKNLCSLFAELLFLIGINRTD 935

Query: 348 QPIACXXXXXXXXXXXXXXXXXTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 407
QPIAC TWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV

Sbjct: 936 QPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMPALIV 995

Query: 408 AVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 467
AVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP

Sbjct: 996 AVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTAILKP 1055

Query: 468 ESGCLDN-----IKSWVIXXXXXXXXXXXXXXXXXXMYINESTVIMAYLFTIFNSLN 518
ESGCLDN IKSWVI MYINESTVIMAYLFTIFNSL

Sbjct: 1056 ESGCLDNINYEDNRPFIKSWVIGAIALLCLLGLTWAFGLMYINESTVIMAYLFTIFNSLQ 1115

Query: 519 GMFIFIFHCVLQKKVRKEYGKCLRTHCCSGKSTESSIGSGKTSGRTPGRYSTGSNSRIR 578
GMFIFIFHCVLQKKVRKEYGKCLRTHCCSG+STESSIGSGKTSGRTPGRYSTGS SRIR

Sbjct: 1116 GMFIFIFHCVLQKKVRKEYGKCLRTHCCSGRSTESSIGSGKTSGRTPGRYSTGSQSRI 1175

Query: 579 RMWNDTVRKQSESSFITGDINSSASLNR----- 606
RMWNDTVRKQSESSFITGDINSSASLNR

Sbjct: 1176 RMWNDTVRKQSESSFITGDINSSASLNRGAMANHLISNALLRPHGTNPNPYNTLLGEP 1235

Query: 607 -----EGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVQIIDRGYNHNE 655
EGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVQIIDRGYNHNE

Sbjct: 1236 NNPSVSMYNAQEGLLNARDTSVMDTLPNGNHGNSYSIASGEYLSNCVQIIDRGYNHNE 1295



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NCBI Conserved Domain Search

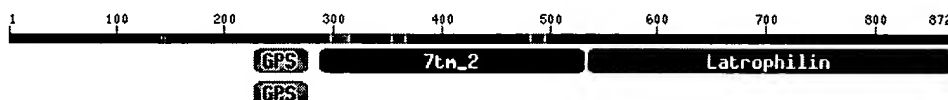
[New Search](#) [PubMed](#) [Nucleotide](#) [Protein](#) [Structure](#) [CDD](#) [Taxonomy](#) [Help?](#)

RPS-BLAST 2.2.3 [Apr-24-2002]

Query= local sequence:
(872 letters)

Database: oasis_sap.v1.58
4540 PSSMs; 885,521 total columns

Click on boxes for multiple alignments



Show Domain Relatives

PSSMs producing significant alignments:

Score E
(bits) value

gnl CDD 2865 pfam02354, Latrophilin, Latrophilin Cytoplasmic C-terminal reg...	485	2e-138
gnl CDD 571 pfam00002, 7tm_2, 7 transmembrane receptor (Secretin family)	217	2e-57
gnl CDD 2352 pfam01825, GPS, Latrophilin/CL-1-like GPS domain. Domain prese...	75.4	8e-15
gnl CDD 3874 smart00303, GPS, G-protein-coupled receptor proteolytic site d...	74.3	2e-14

[gnl|CDD|2865](#), pfam02354, Latrophilin, Latrophilin Cytoplasmic C-terminal region. This family consists of the cytoplasmic C-terminal region in latrophilin. Latrophilin is a synaptic Ca²⁺ independent alpha-latrotoxin (LTX) receptor and is a novel member of the secretin family of G-protein coupled receptors that are involved in secretion. Latrophilin mRNA is present only in neuronal tissue. Latrophillin interacts with G-alpha O.

CD-Length = 370 residues, 100.0% aligned
Score = 485 bits (1250), Expect = 2e-138

Query: 535	KEYGKCLR-THCCSGKSTESSIGSGKTSRTPGRYSTGSNSRIRRMWNDTVRKQSESSF	593
Sbjct: 1	KEYHKCSRGPCCSGLPTESQKDSGKQSGSRTPRLYSTGCQSRIRRMWNDTVRKQSESSF	60
Query: 594	ITGDINSSASLNR-----EGLL	610
Sbjct: 61	IAGDINSTPTLNRGTMGNHLLTNPLLRPHGTNNPYNTLLAESVVCNPPSPPPVFNSPGSYL	120
Query: 611	NNARDTSVMDTLPLNGNHGNSYSIASGEYLSNCVQIIDRGYNHNETALEKKILKELTSNY	670
Sbjct: 121	NNGRDTSGMIDLPLNGNFNNSYLSRSGDYPPGDVQEPDRGRNLNDTAFEKMIISELVHNN	180
Query: 671	IPSYLNNHERSSEQNRNLMNKLVNNLGSGREDDAIVLDDATSFNHEESLGLLELIHEESDA	730
Sbjct: 181	LRGASGGHK--GPPPEPPVPPVPG--GSVSEDDAIVP-DATSFNHADRAGLELLHKELEA	235
Query: 731	PLLPPRVYSTENHQPHHYTRRRIPQDHSESFFPLLNEHTEDLQSPHRDSLYTSMPTLAG	790
Sbjct: 236	PLLPPRT----AHSLLYQSDRRIPLDESESECTAELTAESRELLQSPGRDSLYTSMPLNRD	291
Query: 791	VAATESVTTSTQTEPPPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSSDGFIVP	850
Sbjct: 292	SPYPESSPEPNEALPPPPAPPGPEDIYYKSMPNLGR---NQLQGYQVRRRGSSDGYIAP	348

Query: 851 PNKDGTTPPEGSSKGPahlVTSL 872
Sbjct: 349 PNKEGPGPEGDGQGPMLVTSL 370

gnl|CDD|571, pfam00002, 7tm_2, 7 transmembrane receptor (Secretin family).

CD-Length = 249 residues, 100.0% aligned
Score = 217 bits (554), Expect = 2e-57

Query: 286 DLLLDVITWVGILLSLVCLLICIFTFCFFRGLNSDRNTIHKNLCSLFAELLFLIGINR 345
Sbjct: 1 ALLLSVIYTVGYSLVCLLLAIAIFLFFRKLRCTRNVIHLNLFSLILRLALSFLIGDAV 60

Query: 346 TDQPIA--CAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESHSRRKYFYLVGYGMP 403
Sbjct: 61 LLNSGGLGCKVVAVFLHYFFLANFFWMLVEGLYLYTLLVETFFSERLRLLWYLLIGWGP 120

Query: 404 ALIVAVSAAVDYRSYGTDKVCWLRDLTYFIWSFIGPATLIIMLNVI FLGIALYKMFHHTA 463
Sbjct: 121 AVVVGIWALVRPKGYGNEGCCWLSNEGFWWIFKGPVLLIILVNFIFFINILRVLVQKLR 180

Query: 464 ILKPESGCLDNIKSWVIGAIALLCGLTWAFGLMYINE-STVIMAYLFTIFNSLNGMFI 522
Sbjct: 181 --SPQTGKTDLYRKLVKSTLVLPLLVGTWILFLFAPESQSSLVFLYLFILNSFQGFV 238

Query: 523 FIFHCVLQKKV 533
Sbjct: 239 AVLYCFLNGEV 249

gnl|CDD|2352, pfam01825, GPS, Latrophilin/CL-1-like GPS domain. Domain present in latrophilin/CL-1, sea urchin REJ and polycystin.

CD-Length = 49 residues, 100.0% aligned
Score = 75.4 bits (185), Expect = 8e-15

Query: 226 FNPNCsfWSYSKRTMTGYWSTNGCRLLTNKTHTTCSNHLTNFAVLMAHVEV 278
Sbjct: 1 SNPICVFWEDESS----GVWSTRGCELVETSKTHTTCSNHLTSFAVLMDVPPN 49

gnl|CDD|3874, smart00303, GPS, G-protein-coupled receptor proteolytic site domain; Present in latrophilin/CL-1, sea urchin REJ and polycystin.

CD-Length = 49 residues, 100.0% aligned
Score = 74.3 bits (182), Expect = 2e-14

Query: 226 FNPNCsfWSYSKRTMTGYWSTNGCRLLTNKTHTTCSNHLTNFAVLMAHVEV 278
Sbjct: 1 FNPICVFWEDESS----GEWSTRGCELLETSSSTHTTCSNHLTSFAVLMDVPPI 49

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